

<110> APPLICANT: Keith G. Weinstock et al.
 <120> TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
 CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
 <130> FILE REFERENCE: 107196.135
 <140> CURRENT APPLICATION NUMBER: US/09/252,691C
 <141> CURRENT FILING DATE: 1999-02-18
 <150> PRIOR APPLICATION NUMBER: US 60/094,145
 <151> PRIOR FILING DATE: 1998-07-24
 <150> PRIOR APPLICATION NUMBER: US 60/074,787
 <151> PRIOR FILING DATE: 1998-02-18
 <160> NUMBER OF SEQ ID NOS: 11326

<210> SEQ ID NO 1394
 <211> LENGTH: 669
 <212> TYPE: DNA
 <213> ORGANISM: Enterobacter cloacae
 <400> SEQUENCE: 1394
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 120
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 180
 gggcgagca cgtgaagga ttattcccc gttcaggag tctacgacg ggcagctctg
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 gacgcgaca gcaagggtc gctggctctt accaatgac gctgctcca ggcagctt
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 669

<210> SEQ ID NO 7056
 <211> LENGTH: 222
 <212> TYPE: PRT
 <213> ORGANISM: Enterobacter cloacae
 <400> SEQUENCE: 7056
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 20 Arg Arg Thr Pro Glu Pro Gln Pro Thr Arg Val Ile Leu Phe Asn Lys
 25
 30
 35 Pro Tyr Asp Val Leu Pro Gln Phe Thr Asp Glu Ala Gly Arg Ser Thr
 40
 45
 50 Leu Lys Asp Phe Ile Pro Val Gln Gly Val Tyr Ala Ala Gly Arg Leu
 55
 60
 65 Asp Arg Asp Ser Glu Gly Leu Leu Val Leu Thr Asn Asp Gly Val Leu
 70
 75
 80
 85 Gln Ala Arg Leu Thr Gln Pro Gly Lys Arg Thr Gly Lys Ile Tyr Tyr
 90
 95
 100 Val Gln Val Glu Gly Glu Pro Asp Asp Ala Ser Leu Ala Lys Leu Arg
 105
 110
 115 Asn Gly Val Thr Leu Asn Asp Gly Pro Thr Leu Pro Ala Gly Ile Glu
 120
 125
 130 Arg Val Asn Glu Pro Glu Trp Leu Trp Pro Arg Asn Pro Pro Ile Arg
 135
 140
 145 Glu Arg Lys Ser Ile Pro Thr Ser Trp Leu Lys Ile Thr Leu Tyr Glu
 150
 155
 160
 165 Gly Arg Asn Arg Gln Val Arg Arg Met Thr Ala His Val Gly Phe Pro
 170
 175
 180 Thr Leu Arg Leu Ile Arg Tyr Ala Met Gly Ser Tyr Thr Leu Asp Ser
 185
 190
 195 Leu Ala Asn Gly Glu Trp Arg Asp Val Thr Pro Lys Glu Asn
 200
 205
 210
 215
 220

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cacgggttg agcattcag ctacagaaa gacacagaa gaacccaga acccagcca
ggcggtgta tactttcaa taaccttac gattattgc ccagtttac gacagagcc
ggcgagaca cgtgaaga cttatccc gtaaggag tctacgagc gggagcttg
gacgagaca gcgagggt gctgtctt accaatgac gctgtctca ggcaggtt
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Ala Ile Met Arg Gln-Leu Ile Thr Pro Glu Asn Thr Met Thr Lys Thr
1 5 10 15
Ser Phe Arg Lys His Arg Val Glu Arg Phe Ser Ser Arg Gln Ala Thr
20 25 30
Arg Arg Thr Pro Glu Pro Gln Pro Thr Arg Val Ile Leu Phe Asn Lys
35 40 45
Pro Tyr Asp Val Leu Pro Gln Phe Thr Asp Glu Ala Gly Arg Ser Thr
50 55 60
Leu Lys Asp Phe Ile Pro Val Gln Gly Val Tyr Ala Ala Gly Arg Leu
65 70 75 80
Asp Arg Asp Ser Glu Gly Leu Leu Val Leu Thr Asn Asp Gly Val Leu
95
Gln Ala Arg Leu Thr Gln Pro Gly Lys Arg Thr Gly Lys Ile Tyr Tyr
100 105 110
Val Gln Val Glu Gly Glu Pro Asp Ala Ser Leu Ala Lys Leu Arg
115 120 125
Asn Gly Val Thr Leu Asn Asp Gly Pro Thr Leu Pro Ala Gly Ile Glu
130 135 140
Arg Val Asn Glu Pro Glu Trp Leu Trp Pro Arg Asn Pro Pro Ile Arg
145 150 155 160
Glu Arg Lys Ser Ile Pro Thr Ser Trp Leu Lys Ile Thr Leu Tyr Glu
165 170 175
Gly Arg Asn Arg Gln Val Arg Arg Met Thr Ala His Val Gly Phe Pro
180 185 190
Thr Leu Arg Leu Ile Arg Tyr Ala Met Gly Ser Tyr Thr Leu Asp Ser
195 200 205
Leu Ala Asn Gly Glu Trp Arg Asp Val Thr Pro Lys Glu Asn
210 215 220

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cacgggtg agcgattcag ctacagacaa gccaccagaa gaacgcagga accccagcca 120
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ggcgagca cgtgaagga ttattatccc gtacagggag tctacgcagc ggacggtctg 240
gatcgagca gcgaggggtc gctgtctctt accaatgacg gctgtctoca ggcagagctt 300
actcagcgg gaacagctac cggaaaatt tactatgtgc agttigaagg cgcgcggac 360
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gagctaaat ccatctctac cagctgtgctt aaatcacccc ttatgaagg ccgcaaccca 540
cagctcagg ccatgactgc gcatgtgggc ttccctaccc tgcgactcat tcgctaagcc 600
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gagaactga 669

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Ala Ile Met Arg Gln Leu Ile Thr Pro Glu Asn Thr Met Thr Lys Thr 15
1 Ser Phe Arg Lys His Arg Val Glu Arg Phe Ser Arg Gln Ala Thr 30
Arg Arg Thr Pro Glu Pro Gln Pro Thr Arg Val Ile Leu Phe Asn Lys 45
35 40 45
Pro Tyr Asp Val Leu Pro Gln Phe Thr Asp Glu Ala Gly Arg Ser Thr 60
50 55 60
Leu Lys Asp Phe Ile Pro Val Gln Gly Val Tyr Ala Ala Gly Arg Leu 75
65 70 75
Asp Arg Asp Ser Glu Gly Leu Leu Val Leu Thr Asn Asp Gly Val Leu 80
85 90 95
Gln Ala Arg Leu Thr Gln Pro Gly Lys Arg Thr Gly Lys Ile Tyr Tyr 100
100 105 110
Val Gln Val Glu Gly Glu Pro Asp Asp Ala Ser Leu Ala Lys Leu Arg 115
120 125
Asn Gly Val Thr Leu Asn Asp Gly Pro Thr Leu Pro Ala Gly Ile Glu 130
135 140
Arg Val Asn Glu Pro Glu Trp Leu Trp Pro Arg Asn Pro Pro Ile Arg 145
150 155 160
Glu Arg Lys Ser Ile Pro Thr Ser Trp Leu Lys Ile Thr Leu Tyr Glu 165
170 175
Gly Arg Asn Arg Gln Val Arg Arg Met Thr Ala His Val Gly Phe Pro 180
185 190
Thr Leu Arg Leu Ile Arg Tyr Ala Met Gly Ser Tyr Thr Leu Asp Ser 195
200 205
Leu Ala Asn Gly Glu Trp Arg Asp Val Thr Pro Lys Glu Asn 210
215 220

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cacg99gttg agcgattcag ctacgacaa gccaccagaa gaacccaga acccagccc
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Ser Phe Arg Lys Lys Arg Val Glu Arg Phe Ser Arg Gln Ala Thr
Arg Arg Thr Pro Glu Pro Gln Pro Thr Arg Val Ile Leu Phe Asn Lys
Pro Tyr Asp Val Leu Pro Gln Phe Thr Asp Glu Ala Gly Arg Ser Thr
Leu Lys Asp Phe Ile Pro Val Gln Gly Val Tyr Ala Ala Gly Arg Leu
65
Asp Arg Asp Ser Glu Gly Leu Leu Val Leu Thr Asn Asp Gly Val Leu
85
Gln Ala Arg Leu Thr Gln Pro Gly Lys Arg Thr Gly Lys Ile Tyr Tyr
100
Val Gln Val Glu Gly Glu Pro Asp Asp Ala Ser Leu Ala Lys Leu Arg
115
Asn Gly Val Thr Leu Asn Asp Gly Pro Thr Leu Pro Ala Gly Ile Glu
130
Arg Val Asn Glu Pro Glu Trp Leu Trp Pro Arg Asn Pro Pro Ile Arg
145
Glu Arg Lys Ser Ile Pro Thr Ser Trp Leu Lys Ile Thr Leu Tyr Glu
165
Gly Arg Asn Arg Gln Val Arg Arg Met Thr Ala His Val Gly Phe Pro
180
Thr Leu Arg Leu Ile Arg Tyr Ala Met Gly Ser Tyr Thr Leu Asp Ser
195
Leu Ala Asn Gly Glu Trp Arg Asp Val Thr Pro Lys Glu Asn
210